	imber: 00/2//6///	
C	Changed a file from non-ASCII to ASCII Verified by:	(STIC s
C	Changed the margins in cases where the sequence text was "wrapped" down to the next lin	ne.
E	Edited a format error in the Current Application Data section, specifically:	
= a	Edited the Current Application Data section with the actual turned humber. The humber in applicant was the prior application data; or other	putted by the
٩	Added the mandatory heading and subheadings for "Current Application Data".	
=	Edited the "Number of Sequences" field. The applicant spelled out a number instead of usi	ng an integer.
2	Changed the spelling of a mandatory field (the headings or subheadings), specifically:	
3	Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edit	ed were:
r	nserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:	
	Corrected subheading placement. All responses must be on the same line as each subhea applicant placed a response below the subheading, this was moved to its appropriate place	•
ŀ	Inserted colons after headings/subheadings. Headings edited included:	
C	Deleted extra, invalid, headings used by an applicant, specifically:	
ı	Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filena ☐ page numbers throughout text; ☐ other invalid text, such as	
١	Inserted mandatory headings, specifically:	
•	Corrected an obvious error in the response, specifically:	
1	Edited identifiers where upper case is used but lower case is required, or vice versa.	
(Corrected an error in the Number of Sequences field, specifically:	
-	A "Hard Page Break" code was inserted by the applicant. All occurrences had to be delete	
	Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field ac due to a PatentIn bug). Sequences corrected:	
(Other:	

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

DATE: 03/04/96 TIME: 16:50:20

INPUT SET: S9110.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING
2 3	(1)	SEQUENCE LISTING ENTERED
4 5		(i) APPLICANTS: Hauptmann, R.
6		Falkner, E.
7		Bodo, G.
8		VoÃ, T.
9		Maurer-Fogy, I.
10		
11		(ii) TITLE OF INVENTION: Process for Preparing and Purifying
12		alpha-Interferon
13		
14		(iii) NUMBER OF SEQUENCES: 11
15		· · ·
16		(iv) CORRESPONDENCE ADDRESS:
17		(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
18		(B) STREET: 1100 New York Avenue, Suite 600
19		(C) CITY: Washington
20		(D) STATE: D.C.
21		(E) COUNTRY: U.S.A.
22		(F) ZIP: 20005
23		
24		(V) COMPUTER READABLE FORM:
25		(A) MEDIUM TYPE: Floppy disk
26		(B) COMPUTER: IBM PC compatible
27		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
28		(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29		
30		(vi) CURRENT APPLICATION DATA:
31		(A) APPLICATION NUMBER: 08/249,671
32		(B) FILING DATE: 26-MAY-1994
33		(C) CLASSIFICATION:
34		
35		(viii) ATTORNEY/AGENT INFORMATION:
36		(A) NAME: Esmond, Robert W.
37		(B) REGISTRATION NUMBER: 32,893
38		(C) REFERENCE/DOCKET NUMBER: 0652.1350000
39		(in) MRIDGONGUNIGAMION INCODVAMION.
40		(ix) TELECOMMUNICATION INFORMATION:
41		(A) TELEPHONE: (202) 371-2600
42		(B) TELEFAX: (202) 371-2540
43		
44		
45		2) INFORMATION FOR SEC ID NO. 1.

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

DATE: 03/04/96 TIME: 16:50:24

47	
48	(i) SEQUENCE CHARACTERISTICS:
49	(A) LENGTH: 25 base pairs
50	(B) TYPE: nucleic acid
51	(C) STRANDEDNESS: both
52	(D) TOPOLOGY: unknown
53	(4)
54	(ii) MOLECULE TYPE: cDNA
55	(/
56	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 1:
57	
58	CGTCTTCAAG AATTCGAGAT TATCG 25
59	
60	(2) INFORMATION FOR SEQ ID NO: 2:
61	(2) Intolumiton for pag 15 not 2.
62	(i) SEQUENCE CHARACTERISTICS:
63	(A) LENGTH: 56 base pairs
64	(B) TYPE: nucleic acid
65	(C) STRANDEDNESS: both
66	(D) TOPOLOGY: unknown
67	(b) Topologi: diknown
68	(ii) MOLECULE TYPE: cDNA
69	(II) MODECULE TIPE: CDNA
70	
71	(with GROUPVER BEGGETTERTON, GROUP TO NO. 0.
72	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73	GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56
74 75	GACTICAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56
75 76	/2) INDODUMENTON FOR CENTRAL 2.
76 77	(2) INFORMATION FOR SEQ ID NO: 3:
	(i) CHOURNER GUADAGERICATES.
78	(i) SEQUENCE CHARACTERISTICS:
79	(A) LENGTH: 35 base pairs
80	(B) TYPE: nucleic acid
81	(C) STRANDEDNESS: both
82	(D) TOPOLOGY: unknown
83	
84	(ii) MOLECULE TYPE: cDNA
85	
86	
87	
88	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89	
90	ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC 35
91	
92	(2) INFORMATION FOR SEQ ID NO: 4:
93	
94	(i) SEQUENCE CHARACTERISTICS:
95	(A) LENGTH: 34 base pairs
96	(B) TYPE: nucleic acid
97	(C) STRANDEDNESS: both
98	(D) TOPOLOGY: unknown
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

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106	GGCAGA	ATC	AC AT	rgca:	ragg	C AT'	TTGT	AGCA	ATA	G				34			
107										_							
108	(2) IN	IFOF	RMAT	ION I	FOR :	SEQ :	ID N	0: 5	:								
109				: '		- Ī				•							
110	((i)	SEQU	JENCI	E CH	ARAC'	reri:	STIC	S:								
111			(A)) LEI	NGTH	: 16	5 am:	ino a	acid	S							
112			(B)	TYI	PE: 8	amin	ac:	id									•
113			(D)	TOI	POLO	JY:	line	ar	:								
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118	x)	(i)	SEQU	JENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	: 5:						
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131			30					33					00				
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133		5				****	70			501		75			014		80
134	ŭ						. •					, ,					
135	L	eu	Asp	Lys	Phe	Tvr	Thr	Glu	Leu	Tvr	Gln	Gln	Leu	Asn	Asp	Leu	Glu
136						85				- 2	90					95	
137																	
138	A	la	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	Lys
139			_		100		_		_	105					110		-
140																	
141	G	lu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	Leu
142				115					120					125			
143																	
144	T	'yr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	Val	Arg
145			130					135					140				
146		_	_														
147			Glu	Ile	Met	Arg		Phe	Ser	Leu	Ser		Asn	Leu	Gln	Glu	
148	1	45					150					155					160
149			_	_	_												
150	L	eu	Arg	Ser	Lys												
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

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153 154	(2)	INF	ORMA	TION	FOR	SEQ	ID :	NO:	6 :								
155						_											
156		(i) SE	OUEN	CE C	HARA	CTER	ISTI	cs:							•	
157		. , –	•	_	ENGT					s							
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159					TRAN												
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162	:	(ii) MO	LECII	r.e. 'r.	VPE:	CDN	Δ									
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170		(xi) SE	OUEN	CE D	ESCR	тртт	ON:	SEO	TD N	0: 6	•					
171		.,	,	×	·	J. V.					•••	•					
172	ጥርጥ	GAT	CTG	ССТ	CAA	ACC	CAC	AGC	CTG	GGT	AGC	AGG	AGG	ACC	TTG	AΤG	48
173		Asp															
174	1	_			5					10		5	••- 5		15		
175	_				•												
176	СТС	CTG	GCA	CAG	ATG	AGG	AGA	ATC	тст	CTT	ጥጥር	TCC	TGC	ጥጥር	AAG	GAC	96
177		Leu															
178	202			20		5	5		25			~~-	-,-	30	, _		
179														•			
180	AGA	CGT	GAC	ттт	GGA	ттт	CCC	CAG	GAG	GAG	ттт	GGC	AAC	CAG	TTC	CAA	144
181		Arg															
182	5	3	35		1			40				1	45				
183																	
184	AAG	GCT	GAA	ACC	ATC	CCT	GTC	CTC	CAT	GAG	ATG	ATC	CAG	CAG	ATC	TTC	192
185	Lvs	Ala	Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe	
186	•	50					55					60					
187																	
188	AAT	CTC	TTC	AGC	ACA	AAG	GAC	TCA	TCT	GCT	GCT	TGG	GAT	GAG	ACC	CTC	240
189	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	Leu	
190	65					70	_				75	_	-			80	
191																	
192	CTA	GAC	AAA	TTC	TAC	ACT	GAA	CTC	TAC	CAG	CAG	CTG	AAT	GAC	CTG	GAA	288
193	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu	
194		_	•		85				•	90				_	95		
195																	
196	GCC	TGT	GTG	ATA	CAG	GGG	GTG	GGG	GTG	ACA	GAG	ACT	CCC	CTG	ATG	AAG	336
197	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	Lys	
198		-		100		-		•	105					110		•	
199																	
200	GAG	GAC	TCC	ATT	CTG	GCT	GTG	AGG	AAA	TAC	TTC	CAA	AGA	ATC	ACT	CTC	384
201		Asp															
202	-	2	115					120	3	4 =			125				
203																	
204	TAT	CTG	AAA	GAG	AAG	AAA	TAC	AGC	CCT	TGT	GCC	TGG	GAG	GTT	GTC	AGA	432
205		Leu															
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

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GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT 480	206 207	130	135	140
Ala clu Ile Met Arg Ser Phe Ser Leu Ser Thr		GCA GAA ATC ATG AGA TCT	TTT TCT TTG TCA ACA	AAC TTG CAA GAA AGT 480
145				
TTA AGA ACT AAG GAA		-		
165 165	211			
215 216 217 218 (2) INFORMATION FOR SEQ ID NO: 7: 219 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 869 base pairs (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 222 (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 223 224 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 233 234 TTGATTGATC AGGTAGAGGG GGGGCTGTAC GAGGTAAAGC CCGAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGGGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGC CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 GCATTCCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 242 243 CTGCCCCAAA CCCACAGCCT GGGTAGCAG AGGACCTGA TGCTCCTGC ACAGATGAGG 420 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAG AGGACCTGA TGGATGTGAT 360 245 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGGACTGAC TTCGGATTC CCAGGAGGAG 480 246 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGGACTGAC TTCGGATGAG ACCCCCAGAGGAG 480 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG GAGGAGAATAC 720 252 AAATTCTACA CTGAACTCTA CCAGGAGTG AATGACCTG TGGATGAGA CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGGAGTG AATGACCTG AAGCCTGTG GAGGAAATAC 720 255 TTCCAAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	212	TTA AGA AGT AAG GAA	•	495
215 216 217 218 (2) INFORMATION FOR SEQ ID NO: 7: 219 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 869 base pairs (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 222 (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 223 224 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 233 234 TTGATTGATC AGGTAGAGGG GGGGCTGTAC GAGGTAAAGC CCGAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGGGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGC CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 GCATTCCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 242 243 CTGCCCCAAA CCCACAGCCT GGGTAGCAG AGGACCTGA TGCTCCTGC ACAGATGAGG 420 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAG AGGACCTGA TGGATGTGAT 360 245 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGGACTGAC TTCGGATTC CCAGGAGGAG 480 246 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGGACTGAC TTCGGATGAG ACCCCCAGAGGAG 480 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG GAGGAGAATAC 720 252 AAATTCTACA CTGAACTCTA CCAGGAGTG AATGACCTG TGGATGAGA CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGGAGTG AATGACCTG AAGCCTGTG GAGGAAATAC 720 255 TTCCAAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	213	Leu Arg Ser Lys Glu		
10	214	-		
217 218 (2) INFORMATION FOR SEQ ID NO: 7: 219 220 (A) LENGTH: 869 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown 224 (D) TOPOLOGY: unknown 225 227 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 233 234 TTGATTGATC AGGTAGAGGG GGGCGTGTAC GAGGTAAAGC CCAACAGCGG ACACATCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGGTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGGTGAGGG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATCGTGT 360 243 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGACCTTGA TGCATCTGGC 420 245 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGAC TTCGGAGTAG 420 245 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGAC TTCCTGGC ACAGATCAGG 420 245 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT TGGATTACGC CCCCTGAGC 600 251 AAATTCTACA CTGAACCTA CCAGCAGCT AATGACCTG AAGCCTGTG GATACAGGGG 660 252 AAATTCTACA CTGAACTCTA CCAGCAGCT AATGACCTG AAGCCTGTG GATACAGGGG 660 253 GTGGGGGTGA CAGAGACTCC CCTGATGAAG AAGAAATACA GCCCTTGTGC CTGGGAGGAT 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGGT 780	215			
19	216	•		
219 (i) SEQUENCE CHARACTERISTICS: 221 (A) LENGTH: 869 base pairs 222 (B) TYPE: nucleic acid 223 (C) STRANDEDNESS: both 224 (D) TOPOLOGY: unknown 225 226 (ii) MOLECULE TYPE: CDNA 227 228 229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTCTCT TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCT TTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGA GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGTT GGGATGAGC CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGCAGGTG AATGACCTG TGCAGTGTG GATCCAGCAG 600 253 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	217			
220	218	(2) INFORMATION FOR SEQ		
(A) LENGTH: 869 DASE PAIRS (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (iii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: (xi)	219			
(A) LENGTH: 869 DASE PAIRS (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (iii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: (xi)		(i) SEQUENCE CHARAC	TERISTICS:	
223 (C) STRANDEDNESS: both 224 (D) TOPOLOGY: unknown 225 226 (ii) MOLECULE TYPE: cDNA 227 228 229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTCCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAG AGGACCTGA TGCATGTGAT 360 245 246 AGAATCTCTC TTTTCTCCTG CTTGAAAGGA AGACCTTGA TGCATGTGAT 360 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGAT GATCCAGCAG 480 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT TCCATGAGAT GATCCAGCAG 540 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTG GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTG CTGGGAGGTT 780		(A) LENGTH: 86	9 base pairs	
224 (D) TOPOLOGY: unknown 225 226 (ii) MOLECULE TYPE: cDNA 227 228 229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCTGGC ACAGATGAGG 420 245 246 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 240 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGTC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGTC GGGATGAGC CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTG GAGAAATAC 720 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTT GAGGAAATAC 720 253 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780				
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226 (ii) MOLECULE TYPE: cDNA 227 228 229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGGG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 AGAATCTCC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGAT GATCCAGCAC 540 249 240 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGTC TCCATGAGAC CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTGT GAGAATAAC 720 255 TTCCAAAGAA TCACTCCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780		(D) TOPOLOGY:	unknown	
227 228 229 230		/// VOTEGUE		
228 229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGC CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 240 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT GGGATGAGAC CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTT GATACAGGGG 660 251 CTGGGGGGTGA CAGAGACTCC CCTGATGAGA GAGGACTCA TTCTGGCTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780		(11) MOLECULE TYPE:	CDNA	•
229 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 233 234 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 235 236 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 238 AAAGTTAATC TTTTCAACAG CTGTCATAAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTT GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGAAAATAC 720 255 TTCCAAAGAA TCACTCTCA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780				
230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: 231 232 233 234 235 236 237 237 238 237 238 238 239 239 230 230 231 231 231 232 235 236 236 237 237 238 237 238 238 239 239 239 239 239 230 231 231 231 231 232 232 233 234 235 236 237 238 237 238 238 239 239 239 239 239 240 240 241 241 242 240 241 242 241 242 241 242 242 243 243 243 244 244 245 245 245 246 247 248 247 248 248 247 248 248 247 250 248 247 250 251 251 252 253 254 255 255 255 255 255 256 257 257 258 257 258 257 258 258 258 258 258 258 258 258 258 258				
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GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 AAAGTTAATC TTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 CGCATTCCTC TTGCATCAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 AGAATCTCT TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTC CCAGGAGGAG 480 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTC TCCATGAGAT GATCCAGCAG 540 TTTGGCAACC AGTTCCAACA CCAGCCTG AAAGGACTCA TCCATGAGAT GATCCAGCAG 540 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT GGGATGAGAC CCTCCTAGAC 600 AAATTCTACA CTGAACCTCA CCAGAGCTG AATGACCTG AAGCCTGTG GAGAAATAC 720 TTCCAAAAGAA TCACTCTTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 TTCCAAAAGAA TCACTCTTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	-	(XI) SEQUENCE DESCRI	IFIION: SEQ ID NO: /:	
TTGATTGATC AGGTAGAGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC 120 35 GACGATACGG AGCTGCTGC CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180 237 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 CTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTTC TTGCATCAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT GGGATGAGC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTG AAGCCTGTG GAGGAAATAC 720 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780		GAATTCGAGA TTATCGTCAC T	CAATCCTT CCCAATATCC	CGCAAAATGA CCAACAGCGG 60
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AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT 240 239 240 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257				
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239 240 GTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC 300 241 242 GCATTTCTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCT GGGATGAGC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	237			
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GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360 243 244 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420 245 246 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG 480 247 248 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540 249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC 600 251 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780	239	•		
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249 250 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660 253 254 GTGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257		THE COLLAGE ACTUALIST COLLAGE	CTC A A A CC A TCC CTCTCTCC	TOO DO TO THE TAIL OF THE TAIL
ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC 600 251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257		TITIGGCAACC AGTICCAAAA GC	CIGARACC AICCCIGICC	TCCATGAGAT GATCCAGCAG 540
251 252 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660 253 254 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257		ልጥርጥጥርል ልጥር ጥርጥጥር ልርር ል ር ል <i>ኒ</i>	מככוריים יירייפרייפריים	GGGATGAGAC CCTCCTAGAC 600
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253 254 GTGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257		AAATTCTACA CTGAACTCTA CC	AGCAGCTG AATGACCTCG	AAGCCTGTGT GATACAGGGG 660
254 GTGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720 255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257				
255 256 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780 257		GTGGGGGTGA CAGAGACTCC CC	TGATGAAG GAGGACTCCA	TTCTGGCTGT GAGGAAATAC 720
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257		TTCCAAAGAA TCACTCTCTA TO	TGAAAGAG AAGAAATACA	GCCCTTGTGC CTGGGAGGTT 780
258 GTCAGAGCAG AAATCATGAG ATCTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA 840				
	258	GTCAGAGCAG AAATCATGAG AT	CTTTTTCT TTGTCAACAA	ACTTGCAAGA AAGTTTAAGA 840

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

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This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

		containing ERRORS.
1	·	SEQUENCE LISTING Information: APPLICANTS: Hauptmann, R. Falkner, E. Bodo, G. Voã, T. Maurer-Fogy, I. Corrected Diskette Needed
2	(1) General	Information:
4 5 6	(i)	APPLICANTS: Hauptmann, R. Falkner, E.
7		Bodo, G. Does Not Comply
8	·	Voã, T. Corrected Diskette Needed
9		Maurer-Fogy, I.
10 11 12	(ii)	TITLE OF INVENTION: Process for Preparing and Purifying alpha-Interferon
13 14	(iii)	NUMBER OF SEQUENCES: 11
15 16	(iv)	CORRESPONDENCE ADDRESS:
17	(14)	(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
18		(B) STREET: 1100 New York Avenue, Suite 600
19		(C) CITY: Washington
20		(D) STATE: D.C.
21		(E) COUNTRY: U.S.A.
22		(F) ZIP: 20005
23 24	(**)	COMPUMED DEADARIE FORM.
25	(🗸)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk
26		(B) COMPUTER: IBM PC compatible
27		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
28		(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29		
30	(vi)	CURRENT APPLICATION DATA:
31		(A) APPLICATION NUMBER: 08/249,671
32		(B) FILING DATE: 26-MAY-1994
33 34		(C) CLASSIFICATION:
34 35	/wiii\	ATTORNEY/AGENT INFORMATION:
36	(\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	(A) NAME: Esmond, Robert W.
37		(B) REGISTRATION NUMBER: 32,893
38		(C) REFERENCE/DOCKET NUMBER: 0652.1350000
39	•	
40	(ix)	TELECOMMUNICATION INFORMATION:
41		(A) TELEPHONE: (202) 371-2600
42		(B) TELEFAX: (202) 371-2540
43		
44		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

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ERRORED SEQUENCES FOLLOW:

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	173	48	GAI	CIG	CCI	CAA	ACC	CAC	AGC	C10		AGC	AGG	AGG	ACC		****
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	177	CTC	CTG	CCA	CAG	λጥር	AGG	AGA	ልሞሮ	ጥርጥ	СФФ	ጥጥር	חיכים	יי מר	መጥር	AAG	GAC -
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	179		Leu	Δla	Gln	Met	Ara	Δra	Tle	Ser	Leu	Phe	Ser	Cvs	T.e.11	I.vs	Asn
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	186								- •								
	187	ΔAG	GCT	GAA	ACC	ΔТС	сст	GTC	CTC	САТ	GAG	ΑТС	АТС	CAG	CAG	ATC	ттс
	188	192					•••		•••								
	189		Ala	Glu	Thr	Tle	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe
	190	-1-	50					55					60				
	191												• •				
	192	ААТ	CTC	TTC	AGC	ACA	AAG	GAC	TCA	тст	GCT	GCT	TGG	GAT	GAG	ACC	CTC
	193	240															
	194		Leu	Phe	Ser	Thr	ī.vs	Asp	Ser	Ser	Ala	λla	Trp	Asp	Glu	Thr	Leu
	195	65					70	P				75	P				80
	196	0.5					, ,										
	197	СТА	GAC	ΔΔΔ	ጥጥር	TAC	АСТ	GAA	CTC	TAC	CAG	CAG	СТС	ААТ	GAC	СТС	GAA
	198	288	J.10								0						~
	199		Asp	I.vs	Phe	Tur	Thr	Glu	Leu	Tur	Gln	Gln	Leu	Asn	Asp	Leu	Glu
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		HAPOT SET: SYTTO. TUW
	201 202	GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
	202	336
	204	Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
	205	100 105 110
	206	100 103 110
	207	GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
	207	384
	209	Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
	210 211	115 120 125
	.212	MAM CMC 333 CAC 334 MAC 300 CCM MCM CCC MCC CAC CMM CMC 3C3
	213	TAT CTG AAA GAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
	214 215	Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg 130 135 140
	216	130 135 140
	217	
	217	GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
	218	Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
	220	145 150 155 160
	221	145 150 155 160
	222	TTA AGA AGT AAG GAA
	223	495
	224	Leu Arg Ser Lys Glu
	225	165
	226	103
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	230	
	231	(i) SEQUENCE CHARACTERISTICS:
>	232	(A) LENGTH: 869 base pairs
	233	(B) TYPE: nucleic acid
	234	(C) STRANDEDNESS: both
	235	(D) TOPOLOGY: unknown
	236	
	237	(ii) MOLECULE TYPE: cDNA
	238	
	239	
	240	
	241	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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	243	GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
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	246	TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
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	249	GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
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	255	GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC
	256	300
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	258	GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT
	259	360
	260	
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	262	420
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	265	480
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•	267	TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG
	268	540
	269	
	270	ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC
	271	600
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	273	AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG
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	277	720
	278	
	279	TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT
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	282	GTCAGAGCAG AAATCATGAG ATCTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA
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	285	AGTAAGGAAT GATAACGATC GTAACTGCA
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	288	(2) INFORMATION FOR SEQ ID NO: 8:
	289	(-/
	290	(i) SEQUENCE CHARACTERISTICS:
>	291	(A) LENGTH: 1177 base pairs
-	292	(B) TYPE: nucleic acid
	293	(C) STRANDEDNESS: both
	294	(D) TOPOLOGY: unknown
	295	(2) 101020011 4
	296	(ii) MOLECULE TYPE: cDNA
	297	(11) 1.0000000 11100 0011.
	298	
	299	(ix) FEATURE:
	300	(A) NAME/KEY: CDS
	301	(B) LOCATION: 286873
	302	(D) OTHER INFORMATION: /function= "Cytokine"
	303	/product= "Interferon-omegal"
	304	, product intorroran omegar

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306			(2	A) N	AME/	KEY:	mat	pep	tide							•
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308			Ċ	D) O'	THER	INF	ORMA'	TION	: /f	unct.	ion=	"Cy	toki	ne"		
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311		(ix) FE	ATURI	E:											
312		,	•	A) N		KEY:	sia	pep	tide							
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321		ATTG	ATC A	AGGTZ	AGAGG	ای یاد	الالالالالا	IGIA	GA	JG I A	AAGC	CCG	AIGC	CAG	CATI	CCTGAC
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324		JATA(JGG A	AGCT	3C.I.G.	JG C	GATTI	ACGT	A AA	JAAG	I'I'A'I'	TGA	AGCA.	ree .	regre	CAGTAA
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335		ATC	GCA	TTT	CTT	CTT	GCA	TCT	ATG	TTC	GTT	$\mathbf{T}\mathbf{T}\mathbf{T}$	TCT	ATT	GCT	ACA
336	342	_	_	_			_			_	_	_		_	_	_
337		Ile	Ala	Phe	Leu		Ala	Ser	Met	Phe		Phe	Ser	Ile	Ala	
338	-20					-15					-10					-5
339																
340		GCC	TAT	GCA	TGT	GAT	CTG	CCT	CAG	AAC	CAT	GGC	CTA	CTT	AGC	AGG
341	390															
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343					1				5					10		
344																
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346	438															
347	Asn	Thr	Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile	Ser	Pro	Phe	Leu
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349																
350	TGT	CTC	AAG	GAC	AGA	AGA	GAC	TTC	AGG	TTC	CCC	CAG	GAG	ATG	GTA	AAA
351	486															
352	Cys	Leu	Lys	Asp	Arg	Arq	Asp	Phe	Arq	Phe	Pro	Gln	Glu	Met	Val	Lys
353	4	30	4 -			- 3	35		- 3			40				-
354																
355	GGG	AGC	CAG	TTG	CAG	AAG	GCC	CAT	GTC	ATG	TCT	GTC	СТС	CAT	GAG	ATG
356	534															
357		Ser	Gln	Leu	Gln	Lvs	Δla	His	Val	Met	Ser	Val	Leu	His	Glu	Met
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359																
360	CTG	CAG	CAG	ATC	TTC	AGC	CTC	TTC	CAC	ACA	GAG	CGC	TCC	тст	GCT	GCC
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365		AAC	ATG	ACC	CTC	CTA	GAC	CAA	CTC	CAC	ACT	GGA	CTT	CAT	CAG	CAA
366	630				. •										,	
367	Trp	Asn	Met	Thr	Leu	Leu	Asp	Gln	Leu	His	Thr	Gly	Leu	His	Gln	Gln
368				80					85					90		
369																
370	CTG	CAA	CAC	CTG	GAG	ACC	TGC	TTG	CTG	CAG	GTA	GTG	GGA	GAA	GGA	GAA
371	678															
372			His	T.011	Glu	Thr	Cvs	T.011	T.011	Gln	Val	Val	G] v	Glu	Gly	Glu
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376	726	_	_	_	_				_		_					_
377	Ser	Ala	Gly	Ala	Ile	Ser	Ser	Pro	Ala	Leu	Thr	Leu	Arg	Arg	Tyr	Phe
378		110					115					120				
379																
380	CAG	GGA	ATC	CGT	GTC	TAC	CTG	AAA	GAG	AAG	AAA	TAC	AGC	GAC	TGT	GCC
381	774															
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386	822	GAA	311	GIC	AGA	AIG	OAA	AIC	AIG	ллл	100	110	110		ICA	ACA
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389																
390		ATG	CAA	GAA	AGA	CTG	AGA	AGT	AAA	GAT	AGA	GAC	CTG	GGC	TCA	TCT
391	870															
392	Asn	Met	Gln	Glu	Arg	Leu	Arg	Ser	Lys	Asp	Arg	Asp	Leu	Gly	Ser	Ser
393				160					165					170		
394																
395	TGA	AATG	ATT (CTCA?	rtga:	rt A	ATTT	GCCA!	TA 7	AACAG	TTG	CAC	ATGT	SAC !	CTG	TCAAT
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404			CAT '	TTAT:	TTTT?	AC TO	CATT	'TTAT	' AT'	rctt <i>i</i>	CAT	TTT	ATCAT	TAT	rtat <i>i</i>	CTATT
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407	TAT	ATTC:	TA !	TATA	ACAA	AT G	r t tg(CTT	C AC	ATTGT	TTAT	AAG!	ATAAC	CAA A	AACAI	GTTCA
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671A

DATE: 03/04/96 TIME: 15:06:14

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517	390								_	_						
518	Asn	Ala	Tyr	Ala	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu	Gly	Ser	Arg
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521	AGG	ACC	TTG	ATG	CTC	CTG.	GCA	CAG	ATG	AGG	AGA	ATC	TCT	CTŢ	TTC	TCC
522	438															
523	Arg	Thr	Leu	Met	Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser	Leu	Phe	Ser
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526	TGC	TTG	AAG	GAC	AGA	CGT	GAC	TTT	GGA	TTT	CCC	CAG	GAG	GAG	TTT	GGC
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541	GAT	GAG	ACC	CTC	CTA	GAC	AAA	TTC	TAC	ACT	GAA	CTC	TAC	CAG	CAG	CTG
542	630															
543	Asp	Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu
544				80					85					90		
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570	Leu Gln G	3lu Ser	Leu Arg	Ser Ly	s Glu		
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/08/249,671A*

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Line	Error	Original Text
157 232 291 467	Entered (495) and Calc. Seq. Length (0) differ Entered (869) and Calc. Seq. Length (0) differ Entered (1177) and Calc. Seq. Length (0) differ Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs(A) LENGTH: 869 base pairs(A) LENGTH: 1177 base pairs(A) LENGTH: 879 base pairs